

IN THE SPECIFICATION

[0054] By the term "homologs" is meant structurally similar genes contained within a given species, orthologs are functionally equivalent genes from a given species or strain, as determined for example, in a standard complementation assay. Thus, a polypeptide of interest can be used not only as a model for identifying similar genes in given strains, but also to identify homologs and orthologs of the polypeptide of interest in other species. The orthologs, for example, can also be identified in a conventional complementation assay. In addition or alternatively, such orthologs can be expected to exist in bacteria (or other kind of cells) in the same branch of the phylogenic tree, as set forth, for example, at <ftp://ftp.cmc.msu.edu/pub/rdp/SSU-rRNA/SSU/Prok.phyle> known websites.

[0092] Protein-protein interactions can also be detected using complementation assays such as those described by Pelltier et al at <http://www.abrf.org/JBT/Articles/JBT0012/jbt0012.html>, known websites, WO 00/07038 and WO98/34120.

[0235] For each bait, the previous protocol leads to the identification of prey polynucleotide sequences. Using a suitable software program (e.g., Blastwun, available on the Internet site of the University of Washington) <http://bioweb.pasteur.fr/seqanal/interfaces/blastwu.html> the identity of the mRNA transcript that is encoded by the prey fragment may be determined and whether the fusion protein encoded is in the same open reading frame of translation as the predicted protein or not.